



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/759,179
Source: FWS
Date Processed by STIC: 1/29/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

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Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03



IFWO

RAW SEQUENCE LISTING

DATE: 01/29/2004

PATENT APPLICATION: US/10/759,179

TIME: 15:09:02

Input Set : A:\amended sequence listing.txt

Output Set: N:\CRF4\01292004\J759179.raw

3 <110> APPLICANT: UEMATSU, Chihiro
 4 OKANO, Kazunori
 6 <120> TITLE OF INVENTION: METHOD FOR EXPRESSED GENE ANALYSIS AND PROBE KIT FOR
 EXPRESSED
 7 GENE ANALYSIS
 9 <130> FILE REFERENCE: 1021.43414X00
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/759,179
 C--> 12 <141> CURRENT FILING DATE: 2004-01-20
 14 <150> PRIOR APPLICATION NUMBER: JP 2003-114721
 15 <151> PRIOR FILING DATE: 2003-04-18
 17 <160> NUMBER OF SEQ ID NOS: 24
 19 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

Does Not Comply
 Corrected Diskette Needed

214 <210> SEQ ID NO: 15
 215 <211> LENGTH: 65 *66 shown below*
 216 <212> TYPE: DNA
 217 <213> ORGANISM: Artificial Sequence
 219 <220> FEATURE:
 220 <223> OTHER INFORMATION: Description of Artificial Sequence: reverse DNA primer which
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 221 in NASBA reaction and hybridizes with core gene of hepatitis C virus genotype
 222 I/1a
 224 <400> SEQUENCE: 15
 225 aattctaata cgactcacta tagggccctt ctcactgttc tctcatgagc catcccgccc 60
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 229 <210> SEQ ID NO: 16
 230 <211> LENGTH: 65 *66*
 231 <212> TYPE: DNA
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 235 <223> OTHER INFORMATION: Description of Artificial Sequence: reverse DNA primer which
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 237 II/1b
 239 <400> SEQUENCE: 16
 240 aattctaata cgactcacta tagggcactc atctcttctc cctgttgagc catcctgycc 60
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 244 <210> SEQ ID NO: 17
 245 <211> LENGTH: 65 *66 p.3*
 246 <212> TYPE: DNA
 247 <213> ORGANISM: Artificial Sequence

249 <220> FEATURE:

250 <223> OTHER INFORMATION: Description of Artificial Sequence: reverse DNA primer which
is used

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 252 III/2a
 254 <400> SEQUENCE: 17
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 267 IV/2b
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 276 <212> TYPE: DNA
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 284 <400> SEQUENCE: 19
 285 aattctaata cgactcacta tagggcactc atccctgttc tcttctagga ccggccttcg 60
 E--> 286 ctccga 66 ←

VERIFICATION SUMMARY

DATE: 01/29/2004

PATENT APPLICATION: US/10/759,179

TIME: 15:09:03

Input Set : A:\amended sequence listing.txt

Output Set: N:\CRF4\01292004\J759179.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:226 M:252 E: No. of Seq. differs, <211> LENGTH:Input:65 Found:66 SEQ:15
L:241 M:252 E: No. of Seq. differs, <211> LENGTH:Input:65 Found:66 SEQ:16
L:256 M:252 E: No. of Seq. differs, <211> LENGTH:Input:65 Found:66 SEQ:17
L:271 M:252 E: No. of Seq. differs, <211> LENGTH:Input:65 Found:66 SEQ:18
L:286 M:252 E: No. of Seq. differs, <211> LENGTH:Input:65 Found:66 SEQ:19